

Annex 1: Alignment SEQ ID:29 vs Cao SEQ ID:6

CLUSTAL 2.0.10 multiple sequence alignment

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SEQID29      MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
CAOSEQID6    MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
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SEQID29      AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
CAOSEQID6    AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
*****

SEQID29      SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPAPAPAAPSTPAAPKRRG 180
CAOSEQID6    SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPAPAPAAPSTPAAPKRRG 180
*****

SEQID29      SSGAVVXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAKFKEHEYLGN 240
CAOSEQID6    SSGSVV----- 186
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SEQID29      LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV 300
CAOSEQID6    -----

SEQID29      IVANPREEIIVKNKDEEEKLVSNILHXQQLPTALTCLKVKEDEVVSSEKAKDSFNEKRV 360
CAOSEQID6    -----

SEQID29      AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
CAOSEQID6    -----

SEQID29      EKDESSNDDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDE 480
CAOSEQID6    -----

SEQID29      KKIEEKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
CAOSEQID6    -----

SEQID29      VQEACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
CAOSEQID6    -----

SEQID29      VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPFYEEAMSVSLKVSGIKE 660
CAOSEQID6    -----

SEQID29      EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV 720
CAOSEQID6    -----

SEQID29      EDSSPDSEPVDLFSDDSIQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
CAOSEQID6    -----

SEQID29      GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE 840
CAOSEQID6    -----

SEQID29      TETFSDSPIEIIDEFPTLISSKTDTSFSLKAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
CAOSEQID6    -----

SEQID29      PHDSLKNIQPKVEEKISFSDDFSNGSATSXVLLPPDVSAHGHTQAEIESIVKPKVLE 960
CAOSEQID6    -----

SEQID29      KEAEKKLPSTDEKDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020
CAOSEQID6    -----VDLLYWRDIKKTGVVFGASLFLLLSLTVF 215
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SEQID29      SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
CAOSEQID6    SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
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SEQID29 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
CAO ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335

SEQID29 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
CAO YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373
